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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 08-15-02
Searcher: Bergman, J. A.
Terminal time: 2.2
Elapsed time: _____
CPU time: _____
Total time: 3.5
Number of Searches: _____
Number of Databases: 2

Search Site

STC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG

STN

Dialog

AFS

Geninfo

SDC

DARC/Questel

Other: CGN

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Parkin
09/605573

09/605573

~~FILE~~ 'REGISTRY' ENTERED AT 15:39:41 ON 15 AUG 2002
L1 1 S GRETLMQDQQRLNSWGCKGRIICYTSARWH/SQSP

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS
RN 275801-53-1 REGISTRY
CN 135: PN: JP2000157268 SEQID: 69 unclaimed sequence (9CI) (CA INDEX
NAME)
SQL 30

SEQ 1 GRETLMQDQQ RLNSWGCKGR IICYTSARWH
=====

HITS AT: 1-30

REFERENCE 1: 133:55969

~~FILE~~ 'HCAPLUS' ENTERED AT 15:40:58 ON 15 AUG 2002
L2 1 S L1

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:392837 HCAPLUS
DOCUMENT NUMBER: 133:55969
TITLE: Peptide for detection of Group O HIV-1 and use
for diagnosis
INVENTOR(S): Deleys, Robert; Chen, Jan
PATENT ASSIGNEE(S): Ortho-Clinical Diagnostics, Inc., USA
SOURCE: Jpn. Kokai Tokkyo Koho, 103 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000157268	A2	20000613	JP 1999-338385	19991129
US 6149910	A	20001121	US 1999-433428	19991104
EP 1013766	A2	20000628	EP 1999-309491	19991129

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.:
US 1998-110292P P 19981130
US 1999-119138P P 19990208
US 1999-433428 A 19991104

AB Disclosed are the peptides derived from the immunodominant region of the Group O HIV-1 gp41 envelope protein, which do not correspond to any known naturally occurring Group O sequence or variant. The peptides bind to the antibodies to Group O HIV-1. The peptides are useful in detecting antibodies arise from the infection by Group O HIV-1. The peptides may be prepd. in a hybrid form with that of Group M HIV-1.

IT 275801-53-1
RL: PRP (Properties)
(unclaimed sequence; peptide for detection of Group O HIV-1 and use for diagnosis)

FILE 'HOME' ENTERED AT 15:41:07 ON 15 AUG 2002

Searcher : Shears 308-4994

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 10:11:26 ; Search time 30.17 Seconds

(without alignments)
110.448 Million cell updates/sec

Title: US-09-605-573a-69

Perfect score: 173
Sequence: 1 GRETLMDQDRLNSMCKGRITCYTSARWH 30

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

otal number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	100.0	30	21	AA12264
2	157	90.8	35	21	AA12259
3	157	90.8	149	21	AA12262
4	157	90.8	220	21	AA12261
5	157	90.8	368	21	AA12253
6	157	90.8	439	21	AA12252
7	155	89.6	28	21	AA12257
8	134	77.5	23	21	AA12256
9	133	76.9	23	21	AA12254
10	132	76.3	23	21	AA12255
11	131	75.7	33	21	AA12236

12	131	75.7	40	17	AA12243	Partial sequence o
13	130	75.1	32	19	AA12249	Peptide derived fr
14	130	75.1	33	21	AA12229	Partial sequence o
15	130	75.1	36	21	AA12229	Peptide #6 for det
16	130	75.1	113	20	AA12231	HIV-1 gp41 isol
17	129	74.6	33	21	AA12231	Partial sequence o
18	129	74.6	40	17	AA12231	Partial sequence o
19	128	74.0	33	21	AA12208	Partial sequence o
20	128	74.0	33	21	AA12215	Partial sequence o
21	128	74.0	33	21	AA12215	Partial sequence o
22	128	74.0	33	21	AA12218	Partial sequence o
23	128	74.0	33	21	AA12219	Partial sequence o
24	128	74.0	35	15	AA12219	Partial sequence o
25	128	74.0	35	20	AA12219	Partial sequence o
26	128	74.0	36	20	AA12219	Partial sequence o
27	128	74.0	36	21	AA12219	Partial sequence o
28	128	74.0	36	21	AA12219	Partial sequence o
29	128	74.0	36	21	AA12219	Partial sequence o
30	128	74.0	36	21	AA12219	Partial sequence o
31	128	74.0	167	19	AA12219	Partial sequence o
32	128	74.0	204	15	AA12219	Partial sequence o
33	128	74.0	351	15	AA12219	Partial sequence o
34	128	74.0	351	20	AA12219	Partial sequence o
35	127	73.4	32	22	AA12219	Partial sequence o
36	127	73.4	33	21	AA12219	Partial sequence o
37	127	73.4	36	21	AA12219	Partial sequence o
38	127	73.4	36	21	AA12219	Partial sequence o
39	127	73.4	36	21	AA12219	Partial sequence o
40	127	73.4	36	21	AA12219	Partial sequence o
41	127	73.4	36	21	AA12219	Partial sequence o
42	127	73.4	36	21	AA12219	Partial sequence o
43	127	73.4	111	17	AA12219	Partial sequence o
44	126	72.8	33	21	AA12219	Partial sequence o
45	126	72.8	40	17	AA12219	Partial sequence o

ALIGNMENTS

RESULT 1	
AA12264	standard; peptide: 30 AA.
AA12264	
10-NOV-2000	(first entry)
HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.	
HIV-1, AIDS; human immunodeficiency virus type 1; antibody detection;	
acquired immunodeficiency syndrome; group O HIV; gp41.	
Human immunodeficiency virus type 1.	
EPI013766-A2.	
28-JUN-2000.	
29-NOV-1999;	99EP-0309491.
30-NOV-1998;	98US-0110292.
08-FEB-1999;	99US-0119138.
04-NOV-1999;	99US-0433428.
(ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.	
De Leys R, Zheng J;	
WPI, 2000-402205/35.	
New antigenic peptides and peptide functional derivatives, useful for	
detection of antibodies produced in response to human immunodeficiency	
virus group O antibodies -	


```

XX XX      (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
PA XX
XX XX      De Leys R, Zheng J;
PI XX
DR XX      WPI: 2000-402205/35.
PR XX
PT XX      New antigenic peptides and peptide functional derivatives, useful for
        detection of antibodies produced in response to human immunodeficiency
        virus group O antibodies -
PS XX
PE XX      Example 5; Fig 6; 52pp; English.
CC XX
CC XX      Human Immunodeficiency Virus (HIV) is the principle aetiological
CC XX      agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
CC XX      envelope protein, and may be used as an antigen for the detection of
CC XX      antibodies produced in response to HIV infection. Mosaic gp41 proteins
CC XX      were constructed, in which the immunodominant region of group M HIV was
CC XX      replaced by the corresponding region from group O HIV. The mosaic gp41
CC XX      proteins would be useful as antigens, used in the detection of anti-group
CC XX      O HIV antibodies produced in response to HIV infection. The present
CC XX      sequence is a dithyrotolate reductase (DHFR) fusion protein of one such
CC XX      mosaic protein.
SQ XX
SQ XX      Sequence    439 AA:

Query Match          90.8%; Score 157; DB 21; Length 439;
Best Local Similarity 96.4%; Pred. No. 2.4e-14;
Matches   27; Conservative    1; Mismatches    0; Indels    0; Gaps    0

OY       3 ETLMDQORLNSWGCKGRITCTSRMH 30
         |||||:|||||:|||||:|||||
Db        240 eElmgngqrlnswgckgrilcytsarwh 267

RESULT      7
AAB12257
ID AAB12257 standard; peptide; 28 AA.
XX
XX AAB12257;
AC
DT 10-NOV-2000 (first entry)
XX
DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 3.
XX
XX HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;
XX KW acquired immunodeficiency syndrome; group O HIV; gp41.
XX
XX Human immunodeficiency virus type 1.
XX
FH Misc Location/Qualifiers
FT Misc-difference 6 /note= "Any natural amino acid apart from L-asparagine"
FN EP1013766-A2.
PN 28-JUN-2000.
PD
PP 29-NOV-1999; 99EP-0309491.
PX
XX 30-NOV-1998; 98US-0110292.
PR 08-FEB-1999; 99US-0119138.
PR 04-NOV-1999; 99US-0433428.
XX
PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
PI De Leys R, Zheng J;
XX
XX WPI: 2000-402205/35.
DR
PT
XX
XX New antigenic peptides and peptide functional derivatives, useful for
XX detection of antibodies produced in response to human immunodeficiency

```

PT	virus group O antibodies -
XX	
PS	Claim 1; Page 36; 52pp; English.
XX	
CC	The present sequence is a peptide 147 related peptide from Human
CC	Immunodeficiency Virus Type 1 (HIV-1). This sequence is a partial
CC	consensus sequence of the immunodominant region of gp41 protein derived
CC	from a variety of HIV-1 group O (outlier) strains: AN770, WVP5180, VAD,
CC	DUR, POC, FAN, LOB, MAN, NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686,
CC	ABR063, ABR124, ABR1123, ABR2156, 193Ha, CDC7755, CDC1897, HLD28, 1515,
CC	1516, D47-2d, HCT72c, NT42 and PE41 (see AAB12207 to AAB12236). HIV is
CC	the principle aetiological agent for acquired immunodeficiency syndrome
CC	(AIDS). gp41 is a HIV envelope protein, and so the present sequence may
CC	be used as an antigen for the detection of antibodies produced in
CC	response to HIV infection.
XX	
SO	Sequence 28 AA;
XX	
Query Match	89.6%; Score 155; DB 21; Length 28;
Best Local Similarity	96.4%; Pred. No. 2.5e-15;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	3 EHTLMDDQRLNWSGCKGRICYSARWH 30
Db	1 eELmgxqgrlinswgckgrilcytsarwh 28
XX	
RESULT	8
AAB12256	
ID	AAB12256 standard; peptide: 23 AA.
XX	
AC	AAB12256;
XX	
DT	10-NOV-2000 (first entry)
XX	
DE	HIV-1 gp41 immunodominant region consensus sequence peptide 147-4.
XX	
KW	HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;
RW	acquired immunodeficiency syndrome; group O HIV; gp41.
OS	Human immunodeficiency virus type 1.
XX	
PN	EPI013766-A2.
XX	
PD	28-JUN-2000.
XX	
PF	29-NOV-1999; 99EP-0309491.
XX	
PR	30-NOV-1998; 98US-0110292.
PR	08-FEB-1999; 99US-0119138.
BR	04-NOV-1999; 99US-0433428.
XX	
PA	(ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
XX	
PI	De Lays R, Zheng J;
XX	
DR	WPI: 2000-402205/35.
XX	
PT	New antigenic peptides and peptide functional derivatives, useful for
PT	detection of antibodies produced in response to human immunodeficiency
PT	virus group O antibodies -
XX	
PS	Claim 1; Page 36; 52pp; English.
XX	
CC	The present sequence is peptide 147-4 from Human Immunodeficiency Virus
CC	Type 1 (HIV-1). This sequence is a partial consensus sequence of the
CC	immunodominant region of gp41 protein derived from a variety of HIV-1
CC	group O (outlier) strains: AN770, WVP5180, VAD, DUR, POC, FAN, LOB, MAN,
CC	NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABR063, ABR1123,
CC	ABR2156, 193Ha, CDC7755, CDC1897, HLD28, 1515, 1516, D47-2d, HCT72c,
CC	NT42 and PE41 (see AAB12207 to AAB12236). HIV is the principle
CC	aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is

CC a HIV envelope protein, and so the present sequence may be used as an
CC antigen for the detection of antibodies produced in response to HIV
CC infection.
XX
SO Sequence 23 AA;

Query Match 77.5%; Score 134; DB 21; Length 23;
Best Local Similarity 95.7%; Pred. No. 2, 1e-12;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 DOORLNSWGCKGRITCYTSARWH 30
Db 1 egqrlnswgckgrilcytsarwh 23

RESULT 9
AAB12254
ID AAB12254 standard; peptide: 23 AA.

XX AAB12254:
DT 10-NOV-2000 (first entry)

DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 1.

KW HIV-1; AIDS: human immunodeficiency virus type 1; antibody detection;
KM acquired immunodeficiency syndrome; group O HIV; gp41.

OS Human immunodeficiency virus type 1.

XX EPI013766-A2.

XX 28-JUN-2000.

PF 29-NOV-1999; 99EP-0309491.

XX 30-NOV-1998; 98US-0110292.

PR 08-FEB-1999; 99US-0119138.

PR 04-NOV-1999; 99US-0433428.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

PI De Leys R, Zheng J;

DR WPI: 2000-402205/35.

PT New antigenic peptides and peptide functional derivatives, useful for
PT detection of antibodies produced in response to human immunodeficiency
PT virus group O antibodies -

XX Claim 1; Page 35; 52pp; English.

CC The present sequence is peptide 147 of Human Immunodeficiency Virus Type
CC 1 (HIV-1). This sequence is a partial consensus sequence of the
CC immunodominant region of gp41 protein derived from a variety of HIV-1
CC group O (outlier) strains: ANT70, MYP5180, VAN, DUR, POC, FAN, LOB, MAN,
CC NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABR063, ABR124, ABR1123,
CC ABR2156, 193Ha, CDC7755, CDC1897, HUD28, 1515, 1516, D47-2d, HCYT2c,
CC N42 and PE41 (see AAB12207 to AAB12236). HIV is the principle
CC aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is
CC a HIV envelope protein, and so the present sequence may be used as an
CC antigen for the detection of antibodies produced in response to HIV
CC infection.
XX
XX Sequence 23 AA;

Query Match 76.9%; Score 133; DB 21; Length 23;
Best Local Similarity 95.7%; Pred. No. 2, 9e-12;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 DOORLNSWGCKGRITCYTSARWH 30

Db. :|||||
1 ngqrlnswgckgrilcytsarwh 23

RESULT 10

ID AAB12255 standard; peptide: 23 AA.

XX AAB12255:

DT 10-NOV-2000 (first entry)

DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 2.

KW HIV-1; AIDS: human immunodeficiency virus type 1; antibody detection;
KM acquired immunodeficiency syndrome; group O HIV; gp41.

OS Human immunodeficiency virus type 1.

XX Key Location/Qualifiers

FT MISC-difference 1 /note="any natural amino acid apart from L-asparagine"

XX EPI013766-A2.

XX 28-JUN-2000.

PF 29-NOV-1999; 99EP-0309491.

XX 30-NOV-1998; 98US-0110292.

PR 08-FEB-1999; 99US-0119138.

PR 04-NOV-1999; 99US-0433428.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

PI De Leys R, Zheng J;

DR WPI: 2000-402205/35.

PT New antigenic peptides and peptide functional derivatives, useful for
PT detection of antibodies produced in response to human immunodeficiency
PT virus group O antibodies -

XX Claim 1; Page 35; 52pp; English.

CC The present sequence is a peptide 147 related peptide from Human
CC immunodeficiency virus type 1 (HIV-1). This sequence is a partial
CC consensus sequence of the immunodominant region of gp41 protein derived
CC from a variety of HIV-1 group O (outlier) strains: ANT70, MYP5180, VAN,
CC DUR, POC, FAN, LOB, MAN, NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686,
CC ABR063, ABR124, ABR1123, ABR2156, 193Ha, CDC7755, CDC1897, HUD28, 1515,
CC 1516, D47-2d, HCYT2c, N42 and PE41 (see AAB12207 to AAB12236). HIV is
CC the principle aetiological agent for acquired immunodeficiency syndrome
CC (AIDS). gp41 is a HIV envelope protein, and so the present sequence may
CC be used as an antigen for the detection of antibodies produced in
CC response to HIV infection.
XX
XX Sequence 23 AA;

Query Match 76.3%; Score 132; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 DOORLNSWGCKGRITCYTSARWH 30
Db 2 gqrlnswgckgrilcytsarwh 23

RESULT 11
AAB12236
ID AAB12236 standard; peptide: 33 AA.

Sequence 36 AA;

Query Match 75.1%; Score 130; DB 21; Length 36;
 Best Local Similarity 75.0%; Pred. No. 1.3e-11;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 EFLMODQORLNSWGCKGRICYSARWH 30
 |||:||||| |||||:||||| :|:
 Db 8 etliqnggrlnlwckgrilicytclskwn 35

Search completed: August 15, 2002, 10:46:04
 Job time: 2078 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 10:37:56 ; Search time 13.14 Seconds

(without alignments)

55.766 Million cell updates/sec

Title: US-09-605-573A-69

Sequence: 173

1 GRETLMODQORLNSWGCKGRITCYTSARWH 30

Scoring table:

BLOSUM62

Gap 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Optimal number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	100.0	30	US-09-433-428D-69	Sequence 69, Appl
2	166	96.0	30	US-09-433-428D-63	Sequence 63, Appl
3	157	90.8	149	US-09-433-428D-67	Sequence 67, Appl
4	157	90.8	220	US-09-433-428D-66	Sequence 66, Appl
5	157	90.8	368	US-09-433-428D-58	Sequence 58, Appl
6	157	90.8	439	US-09-433-428D-57	Sequence 57, Appl
7	155	89.6	28	US-09-433-428D-64	Sequence 64, Appl
8	155	89.6	35	US-09-433-428D-61	Sequence 61, Appl
9	134	77.5	23	US-09-433-428D-60	Sequence 60, Appl
10	133	76.3	23	US-09-433-428D-60	Sequence 59, Appl
11	131	75.7	40	US-09-433-428D-30	Sequence 30, Appl
12	131	75.7	40	US-08-894-699-36	Sequence 36, Appl
13	131	75.7	40	US-09-433-428D-23	Sequence 23, Appl
14	131	75.7	40	US-09-433-428D-25	Sequence 25, Appl
15	130	75.1	33	US-09-433-428D-23	Sequence 39, Appl
16	129	74.6	40	US-08-894-699-39	Sequence 39, Appl
17	129	74.6	40	US-09-433-428D-2	Sequence 2, Appl
18	128	74.0	33	US-09-433-428D-9	Sequence 9, Appl
19	128	74.0	33	US-09-433-428D-10	Sequence 10, Appl
20	128	74.0	33	US-09-433-428D-12	Sequence 12, Appl
21	128	74.0	33	US-09-433-428D-13	Sequence 13, Appl
22	128	74.0	35	US-08-470-202-62	Sequence 62, Appl
23	128	74.0	35	US-08-471-770-62	Sequence 62, Appl
24	128	74.0	35	US-08-468-059-62	Sequence 62, Appl
25	128	74.0	35	US-09-109-916-62	Sequence 62, Appl
26	128	74.0	35	US-09-109-916-62	Sequence 62, Appl
27	128	74.0	35	US-09-109-916-62	Sequence 62, Appl

ALIGNMENTS

28	128	74.0	146	2	US-08-394-021-10	Sequence 10, Appl
29	128	74.0	146	4	US-09-131-551-10	Sequence 10, Appl
30	128	74.0	204	4	US-08-965-056-105	Sequence 105, Appl
31	128	74.0	351	1	US-08-470-202-46	Sequence 46, Appl
32	128	74.0	351	1	US-08-471-770-46	Sequence 46, Appl
33	128	74.0	351	2	US-08-468-059-46	Sequence 46, Appl
34	128	74.0	351	4	US-09-109-916-46	Sequence 46, Appl
35	127	73.4	33	4	US-09-433-428D-6	Sequence 6, Appl
36	127	73.4	40	3	US-08-894-699-68	Sequence 68, Appl
37	127	73.4	40	4	US-09-444-410-68	Sequence 68, Appl
38	126	72.8	33	4	US-08-894-699-24	Sequence 24, Appl
39	126	72.8	40	3	US-09-433-428D-38	Sequence 38, Appl
40	126	72.8	40	4	US-09-444-410-38	Sequence 38, Appl
41	125	72.3	33	4	US-09-433-428D-20	Sequence 20, Appl
42	125	72.3	40	3	US-08-894-699-41	Sequence 41, Appl
43	125	72.3	40	4	US-09-444-410-41	Sequence 41, Appl
44	125	72.3	356	1	US-08-602-713-12	Sequence 12, Appl
45	125	72.3	356	4	US-08-989-493-12	Sequence 12, Appl

RESULT 1
US-09-433-428D-69
Sequence 69, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 69
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV Consensus
US-09-433-428D-69

Query Match 100.0%; Score 173; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2, 2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRETLMODQORLNSWGCKGRITCYTSARWH 30
DB 1 GRETLMODQORLNSWGCKGRITCYTSARWH 30

RESULT 2
US-09-433-428D-63
Sequence 63, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

NAME/KEY: Xaa is any amino acid
LOCATION: 8
OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
OTHER INFORMATION: Sequence
US-09-433-428D-63

Query Match 96.0%; Score 166; DB 4; Length 30;
Best Local Similarity 96.7%; Pred. No. 2.4e-18;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GRTLMQOORLNSWGCKGRITCYTSARWH 30
|||||
Db 1 GRTLMQOORLNSWGCKGRITCYTSARWH 30

RESULT 3
US-09-433-428D-67
Sequence 67, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentlin Ver. 2.0

SEQ ID NO 67

LENGTH: 149

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:HIV Consensus

OTHER INFORMATION: Sequence

US-09-433-428D-67

Query Match 90.8%; Score 157; DB 4; Length 149;
Best Local Similarity 96.4%; Pred. No. 3.1e-16;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ETLMOOORLNSWGCKGRITCYTSARWH 30
|||||
Db 44 ETLMOOORLNSWGCKGRITCYTSARWH 71

SUIT 4
-09-433-428D-66
Sequence 66, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentlin Ver. 2.0

SEQ ID NO 66

LENGTH: 220

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:HIV Consensus

OTHER INFORMATION: Sequence

US-09-433-428D-66

Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 ETLMOOORLNSWGCKGRITCYTSARWH 30
|||||
Db 44 ETLMOOORLNSWGCKGRITCYTSARWH 71

RESULT 5
US-09-433-428D-58
Sequence 58, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentlin Ver. 2.0

SEQ ID NO 58

LENGTH: 368

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:HIV Consensus

OTHER INFORMATION: Sequence

US-09-433-428D-58

Query Match 90.8%; Score 157; DB 4; Length 368;
Best Local Similarity 96.4%; Pred. No. 8.5e-16;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ETLMOOORLNSWGCKGRITCYTSARWH 30
|||||
Db 240 ETLMOOORLNSWGCKGRITCYTSARWH 267

RESULT 6
US-09-433-428D-57
Sequence 57, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentlin Ver. 2.0

SEQ ID NO 57

LENGTH: 439

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:HIV Consensus

OTHER INFORMATION: Sequence

US-09-433-428D-57

Query Match 90.8%; Score 157; DB 4; Length 439;
Best Local Similarity 96.4%; Pred. No. 1e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ETLMOOORLNSWGCKGRITCYTSARWH 30
|||||
Db 240 ETLMOOORLNSWGCKGRITCYTSARWH 267

RESULT 7
US-09-433-428D-62


```
; Sequence 62, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 62
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 6
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; US-09-433-428D-62
```

```
Query Match          89.6%; Score 155; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 3 ETLMDQORLNSMGCKGRITCYTSARWH 30
DB 1 ETLMDQORLNSMGCKGRITCYTSARWH 28
```

```
RESULT 8
US-09-433-428D-64
; Sequence 64, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 64
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 13
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; US-09-433-428D-64
```

```
Query Match          89.6%; Score 155; DB 4; Length 35;
Best Local Similarity 96.4%; Pred. No. 1.3e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 3 ETLMDQORLNSMGCKGRITCYTSARWH 30
DB 8 ETLMDQORLNSMGCKGRITCYTSARWH 35
```

```
RESULT 9
US-09-433-428D-61
; Sequence 61, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
```

```
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 61
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; US-09-433-428D-61
```

```
Query Match          77.5%; Score 134; DB 4; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.1e-13;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 8 DQORLNSMGCKGRITCYTSARWH 30
DB 1 EQORLNSMGCKGRITCYTSARWH 23
```

```
RESULT 10
US-09-433-428D-59
; Sequence 59, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 59
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; US-09-433-428D-59
```

```
Query Match          76.9%; Score 133; DB 4; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e-13;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 8 DQORLNSMGCKGRITCYTSARWH 30
DB 1 DQORLNSMGCKGRITCYTSARWH 23
```

```
RESULT 11
US-09-433-428D-60
; Sequence 60, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 60
; LENGTH: 23
; TYPE: PRT
```

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Xaa is any amino acid
LOCATION: 1
OTHER INFORMATION: Description of Artificial Sequence: HIV Consensus
OTHER INFORMATION: Sequence
US-09-433-428D-60

Query Match 76.3%; Score 132; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 QOQLNSWGCKGRICYSARWH 30
DB 2 QOQLNSWGCKGRICYSARWH 23

RESULT 12

US-09-433-428D-30

Sequence 30, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:

APPLICANT: De leys, Robert J.

APPLICANT: Zheng, Jian

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 30

LENGTH: 33

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-433-428D-30

Query Match 75.7%; Score 131; DB 4; Length 33;
Best Local Similarity 75.0%; Pred. No. 4.6e-13;
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSWGCKGRICYSARWH 30
DB 6 ETLMDQORLNSWGCKGRICYSARWH 33

RESULT 13

US-08-894-699-36

Sequence 36, Application US/08894699
Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOR

APPLICANT: LOUSSEY-ATAKA, IBITISSAM

APPLICANT: LY, THOI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,699

FILING DATE: 01-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294

FILING DATE: 26-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-894-699-36

Query Match 75.7%; Score 131; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No. 5.7e-13;
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSWGCKGRICYSARWH 30
DB 11 ETLMDQORLNSWGCKGRICYSARWH 38

RESULT 14

US-09-444-410-36

Sequence 36, Application US/09444410
Patent No. 6270975

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOR

APPLICANT: LOUSSEY-ATAKA, IBITISSAM

APPLICANT: LY, THOI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/444,410

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/894,699

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614
 REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-444-410-36

Query Match 75.7% Score 131; DB 4; Length 40;
 Best Local Similarity 75.0% Pred. No. 5.7e-13;
 Matches 21: Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 ETLMDQOORLNSWCGCKGRICYSARWH 30
 DB 11 ETLMDQOORLNSWCGCKGRICYSARWH 38

RESULT 15
 US-09-433-428D-23
 Sequence 23, Application US/09433428D
 Patent No. 6149910
 GENERAL INFORMATION:
 APPLICANT: De Leys, Robert J.
 APPLICANT: Zheng, Jian
 TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 FILE REFERENCE: CBS-207
 CURRENT APPLICATION NUMBER: US/09/433,428D
 CURRENT FILING DATE: 1999-11-04
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 23
 LENGTH: 33
 TYPE: PRT
 ORGANISM: Human Immunodeficiency virus type 1
 US-09-433-428D-23

Query Match 75.1% Score 130; DB 4; Length 33;
 Best Local Similarity 75.0% Pred. No. 6.5e-13;
 Matches 21: Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 ETLMDQOORLNSWCGCKGRICYSARWH 30
 DB 6 ETLMDQOORLNSWCGCKGRICYSARWH 33

Search completed: August 15, 2002, 10:46:23
 Job time: 507 sec

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OM protein - protein search, using sw model

Run on: August 15, 2002, 10:41:11 ; Search time 15.15 Seconds

(without alignments)
190.276 Million cell updates/sec

Title: US-09-605-573a-69

Perfect score: 173

Sequence: 1 GRETLMQDQRLNSMGCKGRITCYTSARWH 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	68.2	104	2	S52930
2	116	67.1	863	2	A53034
3	114	65.9	877	2	S49197
4	93	53.8	854	1	VCLJST
5	92	53.2	858	1	VCLJG2
6	89	51.4	864	1	VCLJG4
7	88	50.9	357	2	S21990
8	88	50.9	358	2	S22002
9	87	50.3	358	2	S22000
10	87	50.3	358	2	S70417
11	87	50.3	859	1	VCLJST
12	86	49.7	151	2	S30448
13	86	49.7	151	2	S30452
14	86	49.7	151	2	S30452
15	86	49.7	151	2	S30452
16	86	49.7	151	2	S30451
17	86	49.7	856	1	A44963
18	85	49.1	151	2	S30457
19	85	49.1	151	2	S30456
20	85	49.1	151	2	S30455
21	85	49.1	151	2	S30454
22	85	49.1	357	2	S22006
23	85	49.1	357	2	S21994
24	85	49.1	357	2	S22004
25	85	49.1	357	2	S21996
26	85	49.1	358	2	S21992
27	85	49.1	358	2	S21998
28	85	49.1	443	2	C41621
29	85	49.1	445	2	A41621

30	85	49.1	454	2	B41621	env polypeptide D
31	85	49.1	843	1	H44001	env polypeptide pr
32	85	49.1	852	1	VCLJBR	env polypeptide pr
33	85	49.1	852	2	T12016	envelope glycoprote
34	85	49.1	853	2	S54384	envelope polypept
35	85	49.1	854	2	S13288	env polypeptide - huma
36	85	49.1	855	1	VCLJH2	env polypeptide pr
37	85	49.1	855	1	VCLJH2	env polypeptide pr
38	85	49.1	856	1	VCLJH3	env polypeptide pr
39	85	49.1	856	1	VCLJH3	env polypeptide pr
40	85	49.1	856	1	VCLJH3	env polypeptide pr
41	85	49.1	859	1	VCLJH3	env polypeptide pr
42	85	49.1	859	1	VCLJH3	env polypeptide pr
43	85	49.1	861	1	VCLJH3	env polypeptide pr
44	85	49.1	861	1	VCLJH3	env polypeptide pr
45	85	49.1	868	1	VCLJH4	env polypeptide - huma

ALIGNMENTS

RESULT 1
S52930
G41 ENV protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C:Accession: S52930
R:Conen, J.H.M.; Guetard, D.; Philbert, F.; Chamaret, S.; Tabary, T.; Montagnier, L.;
submitted to the EMBL Data Library, January 1995
A:Description: A novel HIV-1 strain illustrates the diversity of the O group.
A:Reference number: S52929
A:Accession: S52930
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-104 <COH>
A:Cross-references: EMBL:X84328; NID:9695526; PIDN:CA59066.1; PID:9695527
C:Superfamily: type E retrovirus env polypeptide

Query Match 68.2%; Score 118; DB 2; Length 104;
Best Local Similarity 67.9%; Pred. No. 1.2e-09;
Matches 19; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 ETLMDQDRLNSMGCKGRITCYTSARWH 30
DB 37 ETLMDQDRLNSMGCKGRITCYTSARWH 64

RESULT 2
A53034
gag polypeptide - human immunodeficiency virus type 1 (strain An70)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: A53034
R:Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groe
J.; Virel, 68, 1586-1596, 1994
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African
A:Reference number: A53034; MID:94149849
A:Accession: A53034
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-863 <VAN>
A:Cross-references: GB:L02587
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: polypeptide

Query Match 67.1%; Score 116; DB 2; Length 863;
Best Local Similarity 60.7%; Pred. No. 1.7e-08;
Matches 17; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 3 ETLMDQDRLNSMGCKGRITCYTSARWH 30
DB 37 ETLMDQDRLNSMGCKGRITCYTSARWH 64


```
Query Match      50.9% Score 88; DB 2; Length 357;
Best Local Similarity 50.0%; Pred. NO. 7.2e-05;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
```

```

QY      3  ETLMDQDORLNSMCCRGRIICYSARWH 30
          |||||  |||||  |||||  |||||
Db      86  ERYLKDDQLLGIMCGRLLCTTAVPWN 113

RESULT  9
S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human Immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
:Accession: S22000

```

Query Match	50.3%	Score 87	DB 2	Length 358
Best Local Similarity	50.0%	Pred. No.	0.0001	
Matches 14	Conservative 4	Mismatches 10	Indels 0	Gaps 0
QY	3	ETLMDQRLNSWGCGRILCTYSARWH	30	

Db	86	ERYLDDDLGICWCGRLCTTYXPWN	113	

Query Match	50.3%	Score 87	DB 2	Length 358
Best Local Similarity	50.0%	Pred. NO. 0.0001		
Matches	14	Conservative	4	Mismatches 10
				Indels 0
				Gaps 0
QY	3	ETLMDDQQRILNSWCGCGRIICCTYSARWH	30	
		:::	:::	
DB	86	ERYIKDDQLLGITWGCGRILICCTTYXPWN	113	

```

RESULT 11
VCLIST
env polyprotein precursor - human immunodeficiency virus type 2 (isolate STR)
N:Alternate names: coat polyprotein
N:Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41
C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1994
C:Accession: H33943
R:Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxley, J.A.; Arya, S.K.; Shaw, G.
J. Virol. 64, 890-901, 1990
A:Title: Molecular characterization of an attenuated human immunodeficiency virus type
A:Reference number: A33943; MUID:90112662
A:Accession: H33943
A:Molecule type: genomic RNA
A:Residues: 1-859 <KUN>
A:Cross-references: EMBL:M66924
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1.19/Domain: signal sequence #status predicted <SIG>
F:20-859/Product: env polyprotein #status predicted <ENV>
F:20-501/Product: surface glycoprotein gp120 #status predicted <SGG>

```

F:506-859/Product: transmembrane glycoprotein gp41 #status predicted <TM>
 F:507-523/Region: hydrophobic
 F:675-694/Domain: transmembrane #status predicted <TM>
 F:36,69,78,113,119,131,137,145,160,173,186,200,232,235,242,266,272,283,294,304,359,392,4

Query Match 50.3%; Score 87; DB 1; Length 859;
 Best Local Similarity 48.1%; Pred. No. 0.00023;
 Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 3 ETLMDODORLNSWCGKRIICYSARW 29
 Db 577 EKLKDOAQLNSWGCAROVCHTTVEW 603

RESULT 12

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2
 C>Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
 C:Accession: S30448; S30449; S30480; S30481

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
 A:Reference number: S30448; MUID:92350299

A:Accession: S30448
 A:Molecule type: nucleic acid

A:Residues: 1-151 <GAO>
 A:Cross-references: EMBL:M87069

A:Experimental source: FOENVA13
 A:Accession: S30449

A:Status: preliminary; translation not shown
 A:Molecule type: nucleic acid

A:Residues: 1-151 <GAN>
 A:Cross-references: EMBL:M87071

A:Experimental source: FOENVA3
 R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;

submitted to the EMBL Data Library, December 1992
 A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa

A:Reference number: S30460
 A:Accession: S30480

A:Status: preliminary
 A:Molecule type: nucleic acid

A:Residues: 1-151 <GA2>
 A:Cross-references: EMBL:M87085

A:Accession: S30481
 A:Status: preliminary

A:Molecule type: nucleic acid
 A:Residues: 1-151 <GA3>

A:Cross-references: EMBL:M87076
 C:Genetics:

A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein

Query Match 49.7%; Score 86; DB 2; Length 151;
 Best Local Similarity 48.1%; Pred. No. 6.2e-05;
 Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 3 ETLMDODORLNSWCGKRIICYSARW 29
 Db 28 EKLKDOAQLNSWGCAROVCHTTVEW 54

RESULT 13

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2
 C>Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
 C:Accession: S30453

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
 A:Reference number: S30448; MUID:92350299

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
 A:Reference number: S30448; MUID:92350299

A:Accession: S30453

A:Status: translation not shown
 A:Molecule type: nucleic acid

A:Residues: 1-151 <GAO>
 A:Cross-references: EMBL:M87089

A:Experimental source: FOENVA13
 A:Accession: S30449

A:Status: preliminary; translation not shown
 A:Molecule type: nucleic acid

A:Residues: 1-151 <GAN>
 A:Cross-references: EMBL:M87071

A:Experimental source: FOENVA3
 R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;

submitted to the EMBL Data Library, December 1992
 A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa

A:Reference number: S30460
 A:Accession: S30480

A:Status: preliminary
 A:Molecule type: nucleic acid

A:Residues: 1-151 <GA2>
 A:Cross-references: EMBL:M87085

A:Accession: S30481
 A:Status: preliminary

A:Molecule type: nucleic acid
 A:Residues: 1-151 <GA3>

A:Cross-references: EMBL:M87076
 C:Genetics:

A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein

Query Match 49.7%; Score 86; DB 2; Length 151;
 Best Local Similarity 48.1%; Pred. No. 6.2e-05;
 Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 3 ETLMDODORLNSWCGKRIICYSARW 29
 Db 28 EKLKDOAQLNSWGCAROVCHTTVEW 54

RESULT 15

env protein - human immunodeficiency virus type 2 (fragment)

C:Species: human immunodeficiency virus type 2, HIV-2
 C>Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
 C:Accession: S30450

A:Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
 A:Reference number: S30448; MUID:92350299

A:Accession: S30450
 A:Status: translation not shown

A:Molecule type: nucleic acid
 A:Residues: 1-151 <GAO>

A:Cross-references: EMBL:M87072
 C:Genetics:

A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: coat protein; glycoprotein

Query Match 49.7%; Score 86; DB 2; Length 151;
Best Local Similarity 48.1%; Pred. No. 6.2e-05;
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 3 ETLMDQDQRLNSWCGCKGRITCTYSARW 29
|::|:||||| |::|: |
Db 28 EKYLKDAQQLNSWGCARQVCHTTEW 54

Search completed: August 15, 2002, 10:46:45
Job time: 334 sec

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КАРБОИД	274	274
КАРБОИД	274	274

Query Match	Score 93;	DB 1;	Length 854;
Best Local Similarity	50.0%;	Pred. No. 2.7e-06;	
Matches 14;	Conservative	5;	Mismatches 9; Indels 0; Gaps 0;
3	ETLMDDOORLNSWCGKGRICITYSARWH	30	
1	: : : : : : : : : : : : : : : :	1	
DB	574	ERYILDQDIIILGWCGSKRAVCYTTVPWN	601

Query Match	Best Local Similarity	Score 93;	DB 1;	Length 857;
Matches 15; Conservative	55.6%;	Pred. No. 2.7e-06;	Mismatches 8;	Indels 0; Gaps 0
3 ETLMDQDQRLNSWCGCKGRITCYTSAHW 29	1 : : : : : 1 : : : : :			
Db 575 EKYLDQARLNSWCGCAFRQVCYTTVLIM 601				

RESULT	2			
ENV_HVZKR		STANDARD:	PRT:	857 AA.
ID	ENV_HVZKR			
DT	074126;			
DT	01-NOV-1997 (rel. 35, Last created)			
DT	01-NOV-1997 (rel. 35, Last sequence update)			
DT	15-JUL-1999 (rel. 38, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [Contains: exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 2 (isolate KR) (HIV-2).			
OC	viruses; Retrovirda viruses; Retrovirdae; Lentivirus.			
ON	NCBI_TaxId=73484;			
OX	(1)			
RA	SEQUENCE FROM N.A.			
RA	Kraus G.K., Talbott R., Leavitt M., Luznick L., Schmidt A.,			
RA	Badel P., Bariz C., Morton W., Wong-Straal F., Looney D.;			
RU	Submitted (APR-1995) to the EMBL/Genbank/DDBJ databases.			
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CC	-----			
CC	EMBL; U22047; AAA64582.1; -			
DR	InterPro; IPR000328; Env_GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
DR	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	1	19	POTENTIAL.	
FT	20	503	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	CHAIN	504	TRANSMEMBRANE GLYCOPROTEIN.	
FT	CARBOHYD	36	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	69	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	78	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	113	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	121	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	121	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	134	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	142	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	159	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	186	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	198	N-LINKED (GLCNAC. . .) (POTENTIAL).	

RESULT	3		
ENV_HVZRO	STANDARD:	PRT:	858 AA.
AC	ENV_HVZRO		
P04577:			
DT	13-AUG-1987 (Rel. 05, Created)		
DT	13-AUG-1987 (Rel. 05, last sequence update)		
DT	16-OCT-2001 (Rel. 40, last annotation update)		
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
DE	ENV.		
OS	Human immunodeficiency virus type 2 (isolate ROD) (HIV-2).		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
NC	NCBI_TaxID=11720;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=87173056; PubMed=3031510;		
RA	Guyader M., Emerman M., Sonigo P., Clavel F., Montagnier L.,		
RA	Alizon M.;		
RT	"genome organization and transactivation of the human immunodeficiency virus type 2.";		
RL	Nature 326:662-669(1987).		
CC	-----		
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/		
CC	or send an email to license@isb-sdb.ch).		
CC	-----		
CC	EMBL; M15390; AB000770.1; --		
DR	EMBL; X05291; CA828914.1; --		
DR	PIR; G26262; VCLJG2.		
DR	HIV; M15390; ENV52ROD.		
DR	InterPro: IPR000328; ENV_GP41.		
DR	InterPro: IPR000777; GP120.		
DR	Pfam: PF00515; GP120; 1.		
DR	Pfam: PF00517; GP41; 1.		
DR	AIDS; Coat protein; polypeptide; Glycoprotein; Transmembrane;		
KW	Signal.		
KW	SIGNAL.		
FT	1	17	
FT	CHAIN	501	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	502	TRANSMEMBRANE GLYCOPROTEIN
FT	CAROHWD	34	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CAROHWD	67	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CAROHWD	76	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CAROHWD	76	

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FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 312 312 T -> I (IN REF. 1: AAR0770).
SQ SEQUENCE 858 AA; 98624 MM; C7266AFLF5C5B9A7 CRC64;

```

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Query Match 53.2%; Score 92; DB 1; Length 858;
Best Local Similarity 55.6%; Pred. No. 3.9e-06;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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Oy 3 ETLMOQDQRLNSWCGCKGRICYSARW 29
I :||| ||||| :||| :
Db 583 EKYLDQARLNSWCGAFQVCHTTPW 609

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RESULT 4
ENV_SIVAT STANDARD: PRT; 865 AA.
ID ENV_SIVAT
AC P05886;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
EN ENV.
OS Simian immunodeficiency virus (TVO-1 isolate) (SIV-AGM).
OC Viruses; Retroviral; Retroviridae; Lentivirus.
OX NCBI_TaxID=11731;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88232906; PubMed=3374586;
RA Fukushima M., Miura T., Hasegawa A., Morikawa S., Tsujimoto H.,
RA Miki K., Kitamura T., Hayami M.;
RT "Sequence of simian immunodeficiency virus from African green monkey,
a new member of the HIV/SIV group."
RL Nature 333:457-461(1988).
CC -I- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X07805; CAA30663.2; -.
CC PIR: G30045; VCLG4.
DR

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DR HIV: X07805; ENV$AGMTY.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
KW signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 536 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 537 865 TRANSMEMBRANE GLYCOPROTEIN.
FT SITE 770 770 IN-FRAME TERMINATION CODON.
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 373 373 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 645 645 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 661 661 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 865 AA; 99024 MM; 6CEP0F09001D6D95 CRC64;

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```

Query Match 51.4%; Score 89; DB 1; Length 865;
Best Local Similarity 48.1%; Pred. No. 1.1e-05;
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

```

```

Oy 3 ETLMOQDQRLNSWCGCKGRICYSARW 29
I :||| ||||| :||| :
Db 608 EKYLEDQARLNSWCGAMKOVCHTTEW 634

```

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RESULT 5
ENV_SIVAT STANDARD: PRT; 854 AA.
ID ENV_SIVAT
AC Q02837;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
EN ENV.
OS Simian immunodeficiency virus (isolate AGM / clone GRI-1) (SIV-AGM).
OC Viruses; Retroviral; Retroviridae; Lentivirus.
OX NCBI_TaxID=31684;
RN [1]
RP SEQUENCE FROM N.A.
RX Fomsgaard A., Hirsch V.M., Allan J.S., Johnson P.R.;
RT "A highly divergent proviral DNA clone of SIV from a distinct species
of African green monkey."
RL Virology 182:397-402(1991).
CC -I- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
CC -----
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CC -----

DR EMBL; M56437; AAA91928.1; -

DR EMBL; M58410; AAA47591.1; -

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 24

FT CHAIN 25 522

FT (POTENTIAL).

FT (POTENTIAL).

FT CHAIN 523 854

FT CARBOHYD 35 35

FT CARBOHYD 68 68

FT CARBOHYD 115 115

FT CARBOHYD 136 136

FT CARBOHYD 153 153

FT CARBOHYD 168 168

FT CARBOHYD 182 182

FT CARBOHYD 199 199

FT CARBOHYD 244 244

FT CARBOHYD 255 255

FT CARBOHYD 265 265

FT CARBOHYD 271 271

FT CARBOHYD 283 283

FT CARBOHYD 295 295

FT CARBOHYD 305 305

FT CARBOHYD 355 355

FT CARBOHYD 400 400

FT CARBOHYD 409 409

FT CARBOHYD 458 458

FT CARBOHYD 472 472

FT CARBOHYD 478 478

FT CARBOHYD 623 623

FT CARBOHYD 624 624

FT CARBOHYD 630 630

FT CARBOHYD 646 646

SO SEQUENCE 854 AA; 96855 MW; 5919CA6C9622912F CRC64;

Query Match 50.3%; Score 87; DB 1; Length 854;

Best Local Similarity 48.1%; Pred. No. 2.2e-05;

Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

3 ETLMDQDRLNSWCGKGRITCYTSARW 29

594 EKYLEDQRLNSWCGAKMYCHTTPW 620

RESULT 6

ENV_HV2N2 STANDARD; PRT; 856 AA.

AC P05883;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polyprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 2 (isolate NIH-2) (HIV-2).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11719;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88320359; PubMed=3261862;

RA Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R., Hail L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laue F., Araya S.R., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.;

RT "Genetic variability between isolates of human immunodeficiency virus RT type 2 is comparable to the variability among HIV type 1.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).

CC -----

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CC -----

DR EMBL; J03654; AAB00761.1; -

DR HIV; J03654; ENV52N1H2.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 20

FT CHAIN 21 492

FT CARBOHYD 37 37

FT CARBOHYD 70 70

FT CARBOHYD 79 79

FT CARBOHYD 112 112

FT CARBOHYD 116 116

FT CARBOHYD 128 128

FT CARBOHYD 133 133

FT CARBOHYD 142 142

FT CARBOHYD 182 182

FT CARBOHYD 183 183

FT CARBOHYD 196 196

FT CARBOHYD 228 228

FT CARBOHYD 231 231

FT CARBOHYD 238 238

FT CARBOHYD 262 262

FT CARBOHYD 268 268

FT CARBOHYD 279 279

FT CARBOHYD 290 290

FT CARBOHYD 300 300

FT CARBOHYD 355 355

FT CARBOHYD 390 390

FT CARBOHYD 400 400

FT CARBOHYD 440 440

FT CARBOHYD 457 457

FT CARBOHYD 602 602

FT CARBOHYD 611 611

FT CARBOHYD 627 627

SO SEQUENCE 856 AA; 96665 MW; A938B0A7E2B881D6 CRC64;

Query Match 50.3%; Score 87; DB 1; Length 856;

Best Local Similarity 51.9%; Pred. No. 2.2e-05;

Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

3 ETLMDQDRLNSWCGKGRITCYTSARW 29

574 EKYIKDQRLNSWCGAFRCYCHTSPW 600

RESULT 7

ENV_HV2SB STANDARD; PRT; 846 AA.

AC P12449;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polyprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 2 (isolate SB115) (HIV-2).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11718;

FT DISULFID 125 194 BY SIMILARITY.
 FT DISULFID 130 155 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 328 BY SIMILARITY.
 FT DISULFID 374 435 BY SIMILARITY.
 FT DISULFID 381 408 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96135 MW; 0A901317ED7FE2AB CRC64;

Query Match 49.1%; Score 85; DB 1; Length 847;
 Best Local Similarity 46.4%; Pred. No. 4,4e-05;
 Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 3 ETLMDQORLNSGCKGRITCYTSARWH 30
 Db 575 ERYLRDQDLGIGWCSGKRLCTTVAPWN 602

RESULT 11
 ENV_HY1M2 STANDARD; PRT; 847 AA.
 ID ENV_HY1M2
 AC P05880; 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [contains: exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 CN ENV.
 OS Human immunodeficiency virus type 1 (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D., Salehuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.; "Genetic variation in HIV-1/LAV over time in patients with AIDS or at risk for AIDS."
 RT Science 232:1548-1553(1986).
 RL -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
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DR EMBL: M12507; AB12990.1; -;
 DR HIV: M12507; ENVSMW2.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF005516; GP120; 1.
 DR Pfam: PF005517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Polypeptide; Transmembrane; Signal.
 FT CHAIN 1.
 FT CHAIN 30 501
 FT DISULFID 53 847
 FT DISULFID 118 202
 FT DISULFID 125 193
 FT DISULFID 130 152
 FT DISULFID 215 244
 FT DISULFID 225 236
 FT DISULFID 293 326
 FT DISULFID 372 435
 FT DISULFID 379 408
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96466 MW; CD1E33D73AA5BCAE CRC64;

Query Match 49.1%; Score 85; DB 1; Length 847;
 Best Local Similarity 46.4%; Pred. No. 4,4e-05;
 Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 3 ETLMDQORLNSGCKGRITCYTSARWH 30
 Db 575 ERYLRDQDLGIGWCSGKRLCTTVAPWN 602

RESULT 12
 ENV_HY1B8 STANDARD; PRT; 851 AA.
 ID ENV_HY1B8
 AC P04582; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [contains: exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 97203 MM; 2BB866345DEC915F CRC64;

Query Match 49.1%; Score 85; DB 1; Length 852;
Best Local Similarity 46.4%; Pred. No. 4.4e-05;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSGCKGRICYSARWH 30
DB 580 ERYLDDQDLGIMGCGKLCITTVPMW 607

RESULT 14
ENV_HV1S3 STANDARD: PRT; 852 AA.

AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11690;

RA MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome.";
RL J. Virol. 64:4016-4020(1990).
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DR EMBL: M38427; AAA45067.1; -;
DR HIV: M38427; ENVSP33.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96663 MM; EET7BB8D23C9910D CRC64;

Query Match 49.1%; Score 85; DB 1; Length 852;
Best Local Similarity 46.4%; Pred. No. 4.4e-05;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSGCKGRICYSARWH 30
DB 580 ERYLDDQDLGIMGCGKLCITTVPMW 607

RESULT 15
ENV_HV1MF STANDARD: PRT; 853 AA.

AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11704;

RA MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
RA Wasik A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis.";

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OM protein - protein search, using sw model

Run on: August 15, 2002, 10:46:26 ; Search time 25.26 Seconds

(Without alignments)
205.457 Million cell updates/sec

Title: US-09-605-573a-69

Perfect score: 173

Sequence: 1 GRETLMQDQRLNSWCKGRICYSARWH 30

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 172994929 residues

Minimum number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_archae:.*
2: SP_bacteria:.*
3: SP_fungi:.*
4: SP_human:.*
5: SP_invertebrate:.*
6: SP_mammal:.*
7: SP_mhc:.*
8: SP_organelle:.*
9: SP_phage:.*
10: SP_plant:.*
11: SP_podent:.*
12: SP_virus:.*
13: SP_vertebrate:.*
14: SP_unclassified:.*
15: SP_rvirus:.*
16: SP_bacteriap:.*
17: SP_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	76.9	161	15	O9IEB5
2	133	76.9	324	15	O9IED3
3	132	76.3	179	15	O9IEB4
4	132	76.3	195	15	O9IEB6
5	132	76.3	576	15	O9IEC6
6	131	75.7	219	15	O9IEF1
7	130	75.1	114	15	O9IEC8
8	129	74.6	216	15	O9IEC5
9	129	74.6	219	15	O9IEB5
10	128	74.0	120	15	O9IEB6
11	128	74.0	134	15	O9IEB6
12	128	74.0	134	15	O9IEB6
13	128	74.0	143	15	O9IEB6
14	128	74.0	143	15	O9IEB6
15	127	73.4	876	15	O9IEB6
16	127	73.4	105	15	O9IEB6
			172	15	O9IEB3

17	127	73.4	234	15	O9IEC2	O9IEC2 human immun
18	127	73.4	242	15	O9IEB1	O9IEB1 human immun
19	126	72.8	125	15	O9IEH8	O9IEH8 human immun
20	126	72.8	130	15	O9IEH9	O9IEH9 human immun
21	126	72.8	216	15	O9IEB5	O9IEB5 human immun
22	126	72.8	232	15	O9IEB1	O9IEB1 human immun
23	126	72.8	242	15	O9IEB5	O9IEB5 human immun
24	126	72.8	243	15	O9IEB5	O9IEB5 human immun
25	126	72.8	544	15	O9IEB5	O9IEB5 human immun
26	125	72.3	111	15	O40452	O40452 human immun
27	125	72.3	114	15	O40457	O40457 human immun
28	125	72.3	114	15	O40472	O40472 human immun
29	125	72.3	224	15	O9IEB8	O9IEB8 human immun
30	125	72.3	418	15	O36547	O36547 human immun
31	124	71.7	124	15	O9IEH7	O9IEH7 human immun
32	124	71.7	126	15	O9IEH7	O9IEH7 human immun
33	124	71.7	134	15	O9IEH4	O9IEH4 human immun
34	124	71.7	183	15	O9IEC1	O9IEC1 human immun
35	124	71.7	200	15	O9IEB8	O9IEB8 human immun
36	124	71.7	213	15	O9IEC9	O9IEC9 human immun
37	124	71.7	220	15	O9IEC9	O9IEC9 human immun
38	124	71.7	225	15	O9IEC9	O9IEC9 human immun
39	124	71.7	512	15	O9IEB2	O9IEB2 human immun
40	124	71.7	517	15	O9IEB7	O9IEB7 human immun
41	124	71.7	532	15	O9IEB0	O9IEB0 human immun
42	124	71.7	545	15	O9IEB7	O9IEB7 human immun
43	123	71.1	112	15	O40454	O40454 human immun
44	123	71.1	114	15	O40458	O40458 human immun
45	123	71.1	116	15	O40458	O40458 human immun

ALIGNMENTS

RESULT 1
O9IEB5 PRELIMINARY: PRT: 161 AA.
AC O9IEB5: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP RC STRAIN=BCF57;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.",
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ36405; CAB6253.1; -
DR InterPro: IPR000328; Env_GP41.
KW Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 161 161
SQ SEQUENCE 161 AA; 19305 MW; 5E3AP197E1PDEE7C CRC64;
Query Match
Best Local Similarity 76.9%; Score 133; DB 15; Length 161;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 3 ETLMDQDQRLNSWCKGRICYSARWH 30
Db 31 ETLMDQDQRLNSWCKGRICYSARWH 58
RESULT 2
O9IED3

RESULT 3 PRELIMINARY; PRT; 524 AA.

ID Q91ED3
AC Q91ED3: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 19, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NC NCB1_TaxID=11676;
OX [1]
RN STRAIN=BCF57;
RP SEQUENCE FROM N.A.
RC Roques P., Robertson D., Diamond F., Sousquiere S., Mauciere P.,
RA Deleigne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ133074; CAB96235.1; -
DR EMBL: AJ133074; CAB96235.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.1.
DR Pfam: PF00517; GP41.1.
DR Pfam: PF00517; GP41.1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW NON_TER 1 524
FT NON_TER 1 524
SQ SEQUENCE 524 AA; 59109 MW; C3D9FF12207AE841 CRC64;

Query Match 76.3%; Score 132; DB 15; Length 524;
Best Local Similarity 78.6%; Pred. No. 2.7e-12;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMOOQRLNSWCKGRITCYTSARWH 30
DB 355 ETLMOOQRLNSWCKGRITCYTSARWH 382

RESULT 3 PRELIMINARY; PRT; 179 AA.

ID Q91EB4
AC Q91EB4: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 19, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NC NCB1_TaxID=11676;
OX [1]
RN STRAIN=BCF58;
RP SEQUENCE FROM N.A.
RC Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ236406; CAB96254.1; -
DR EMBL: AJ236406; CAB96254.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41.1.
DR Pfam: PF00517; GP41.1.
DR Transmembrane.1
KW NON_TER 1 179
FT NON_TER 1 179
SQ SEQUENCE 179 AA; 21225 MW; B060634FF1D4531B CRC64;

Query Match 76.3%; Score 132; DB 15; Length 179;
Best Local Similarity 78.6%; Pred. No. 1.2e-12;
Matches 22; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 ETLMOOQRLNSWCKGRITCYTSARWH 30
DB 34 ETLMOOQRLNSWCKGRITCYTSARWH 61

RESULT 4 PRELIMINARY; PRT; 195 AA.

ID Q91EC6
AC Q91EC6: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 19, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NC NCB1_TaxID=11676;
OX [1]
RN STRAIN=BCF06;
RP SEQUENCE FROM N.A.
RC Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ236393; CAB96242.1; -
DR EMBL: AJ236393; CAB96242.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41.1.
DR Pfam: PF00517; GP41.1.
DR Transmembrane.1
KW NON_TER 1 195
FT NON_TER 1 195
SQ SEQUENCE 195 AA; 22964 MW; 2A6363CD0C86A85 CRC64;

Query Match 76.3%; Score 132; DB 15; Length 195;
Best Local Similarity 78.6%; Pred. No. 1.3e-12;
Matches 22; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 ETLMOOQRLNSWCKGRITCYTSARWH 30
DB 35 ETLMOOQRLNSWCKGRITCYTSARWH 62

RESULT 5 PRELIMINARY; PRT; 576 AA.

ID Q91EF1
AC Q91EF1: 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 19, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NC NCB1_TaxID=11676;
OX [1]
RN STRAIN=BCF06;
RP SEQUENCE FROM N.A.
RC Roques P., Robertson D., Diamond F., Sousquiere S., Mauciere P.,
RA Deleigne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ133056; CAB96217.1; -
DR EMBL: AJ133056; CAB96217.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP41.1.
DR Pfam: PF00516; GP41.1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW NON_TER 1 576
FT NON_TER 1 576
SQ SEQUENCE 576 AA; 64977 MW; A21509F3C618195D CRC64;

Query Match 76.3%; Score 132; DB 15; Length 576;
Best Local Similarity 78.6%; Pred. No. 4.3e-12;
Matches 22; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 ETLMOOQRLNSWCKGRITCYTSARWH 30

Db 392 ETLIOMQOORLSMCGKGRITCYTSARWN 419

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RESULT 6
ID 09IEC8 PRELIMINARY; PRT: 219 AA.
AC 09IEC8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF02;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
  "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
  Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ236391; CAB96240.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 219
SO SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;

```

Query Match
Best Local Similarity 75.7%; Score 131; DB 15; Length 219;
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLIOMQOORLSMCGKGRITCYTSARWN 30
Db 48 ETLIOMQOORLSMCGKGRITCYTSARWN 75

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RESULT 7
ID 040456 PRELIMINARY; PRT: 114 AA.
AC 040456;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP O;
RA Bibollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;
  "Molecular characterization of envelope transmembrane glycoprotein of
  14 new human immunodeficiency virus type 1 group O strains from
  different African countries.";
  Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL: Y09772; CA70911.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 114
SO SEQUENCE 114 AA; 13737 MW; 7907F7F5B51FA9D CRC64;

```

Query Match
Best Local Similarity 75.1%; Score 130; DB 15; Length 114;
Matches 21; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 ETLIOMQOORLSMCGKGRITCYTSARWN 30
Db 31 ETLIOMQOORLSMCGKGRITCYTSARWN 58

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RESULT 8
ID 09IEC5 PRELIMINARY; PRT: 216 AA.
AC 09IEC5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF07;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
  "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
  Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ236394; CAB96243.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 216
SO SEQUENCE 216 AA; 25027 MW; 413AE9BBF1B4FC9A CRC64;

```

Query Match
Best Local Similarity 74.6%; Score 129; DB 15; Length 216;
Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLIOMQOORLSMCGKGRITCYTSARWN 30
Db 39 ETLIOMQOORLSMCGKGRITCYTSARWN 66

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RESULT 9
ID 09IEB6 PRELIMINARY; PRT: 219 AA.
AC 09IEB6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF14;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
  "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
  Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ236404; CAB96252.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 219
SO SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

```

Query Match
Best Local Similarity 74.6%; Score 129; DB 15; Length 219;
Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMODQORLNSWCGCKGRITCYTSARWH 30
 DB 49 ETLIONOQRLDLWGCKGRITCYTSVKWN 76

RESULT 10
 ID 011940 PRELIMINARY; PRT: 120 AA.

AC 011940: 01-JUN-1997 (TREMBLrel. 04, Created)
 DT 01-JUN-1997 (TREMBLrel. 04, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

SEQUENCE FROM N.A.
 STRAIN-AGT1123;
 MEDLINE=97340911; PubMed=9197385;
 Brennan C.A., Hackett J. Jr., Zekeng L., Lund J.K., Vallari A.S.,
 Hickman R.K., Guller L., Kaplue L., von Overbeck J., Hampel H.,
 Devare S.G.;
 "Sequence of gp41env immunodominant region of HIV type 1 group O from
 west central Africa."
 AIDS Res. Hum. Retroviruses 13:901-904(1997).
 EMBL: U90133; AAB62816.1;
 InterPro: IPR000328; Env_GP41.
 Pfam: PF00517; GP41; 1.
 DR Transmembrane. 1
 KW NON_TER 120 120
 FT NON_TER 120 120
 SEQUENCE 120 AA; 1463 MW; 22068B4D2822E44 CRC64;

Query Match 74.0%; Score 128; DB 15; Length 120;
 Best Local Similarity 75.0%; Pred. No. 3.2e-12;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMODQORLNSWCGCKGRITCYTSARWH 30
 DB 30 ETLIONOQRLDLWGCKGRITCYTSVKWN 57

RESULT 11
 ID 091H01 PRELIMINARY; PRT: 134 AA.

AC 091H01: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN GP41.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-97CM747;
 MEDLINE=20386754; PubMed=10933623;
 Yang C., Gao F., Fonjunc P.N., Zekeng L., van der Groen G.,
 Plehazek D., Schable C., Lal R.B.;
 "Phylogenetic analysis of protease and transmembrane regions of HIV
 type 1 group O."
 AIDS Res. Hum. Retroviruses 16:1075-1081(2000).
 EMBL: AF229243; AAF71920.1;
 InterPro: IPR000328; Env_GP41.
 Pfam: PF00517; GP41; 1.
 DR Transmembrane. 1
 KW NON_TER 134 134
 FT NON_TER 134 134

SEQUENCE 134 AA; 16066 MW; F6CBF09ABBF87403 CRC64;

Query Match 74.0%; Score 128; DB 15; Length 134;
 Best Local Similarity 75.0%; Pred. No. 3.7e-12;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMODQORLNSWCGCKGRITCYTSARWH 30
 DB 32 ETLIONOQRLDLWGCKGRITCYTSVKWN 59

RESULT 12
 ID 09WRV5 PRELIMINARY; PRT: 143 AA.

AC 09WRV5: 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;

SEQUENCE FROM N.A.
 STRAIN-ESP1;
 MEDLINE=99284364; PubMed=10357472;
 Mas A., Quiñones-Mateu M.E., Domingo E., Soriano V.;
 "Phylogeny of HIV type 1 group O isolates based on env gene
 sequences."
 AIDS Res. Hum. Retroviruses 15:769-773(1999).
 EMBL: AF01814; AAD41226.1;
 InterPro: IPR000328; Env_GP41.
 Pfam: PF00517; GP41; 1.
 DR Transmembrane. 1
 KW NON_TER 143 143
 FT NON_TER 143 143
 SEQUENCE 143 AA; 16325 MW; 1E44A4C631BA10A2 CRC64;

Query Match 74.0%; Score 128; DB 15; Length 143;
 Best Local Similarity 75.0%; Pred. No. 3.9e-12;
 Matches 21; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 ETLMODQORLNSWCGCKGRITCYTSARWH 30
 DB 61 ETLIONOQRLDLWGCKGRITCYTSVKWN 88

RESULT 13
 ID 09WRV4 PRELIMINARY; PRT: 143 AA.

AC 09WRV4: 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ESP2;
 MEDLINE=99284364; PubMed=10357472;
 Mas A., Quiñones-Mateu M.E., Domingo E., Soriano V.;
 "Phylogeny of HIV type 1 group O isolates based on env gene
 sequences."
 AIDS Res. Hum. Retroviruses 15:769-773(1999).
 EMBL: AF01815; AAD41227.1;
 InterPro: IPR000328; Env_GP41.
 Pfam: PF00517; GP41; 1.
 DR

KW Transmembrane.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 16331 MW; 15A17063CD3431D CRC64;

Query Match
Best Local Similarity 74.0%; Score 128; DB 15; Length 143;
Matches 21; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 ETLMDQORLNSWCKGRICVTSARWH 30
DB 61 ETLIONQOLLNMGCKGRICVTSVRWN 88

RESULT 14
079670 PRELIMINARY; PRT; 876 AA.
AC 079670; 01-NOV-1996 (TREMBLrel. 01, Created)
RT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN ENVELOPE PROTEIN GP120/GP41.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94149848; PubMed=8107219;
RA Gurtler L.G., Hauser P.H., Eberle J., von Bruhn A., Knapp S.,
RT Zekeng L., Tsague J.M., Kapteue L.,
RT "A new subtype of human immunodeficiency virus type 1 (MVP-5180) from
Cameroon";
RL J. Virol. 68:1581-1585(1994).
DR EMBL: L20571; AAA44864.1; -;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 876 AA; 99245 MW; A92F868E37522BAB CRC64;

Query Match
Best Local Similarity 71.4%; Score 128; DB 15; Length 876;
Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 3 ETLMDQORLNSWCKGRICVTSARWH 30
DB 596 ETLIONQOLLNMGCKGRICVTSVRWN 623

RESULT 15
011939 PRELIMINARY; PRT; 105 AA.
AC 011939; 01-JUL-1997 (TREMBLrel. 04, Created)
RT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human Immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ABT063;
RX MEDLINE=97340911; PubMed=9197385;
RA Brennan C.A., Hackett J.J., Zekeng L., Lund J.K., Vallari A.S.,
RA Hickman R.K., Gurtler L., Kapteue L., von Overbeck J., Hampl H.,
RA Devare S.G.;
RT "Sequence of gp120env immunodominant region of HIV type 1 group O from

RT west central Africa";
RL AIDS Res. Hum. Retroviruses 13:901-904(1997).
DR EMBL: U90132; AAB62815.1; -;
DR InterPro: IPR000328; Env_GP41.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 12531 MW; 2D3D6B5BADCA4382 CRC64;

Query Match
Best Local Similarity 73.4%; Score 127; DB 15; Length 105;
Matches 20; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 3 ETLMDQORLNSWCKGRICVTSARWH 30
DB 24 ETLMDQORLNSWCKGRICVTSARWH 51

Search completed: August 15, 2002, 10:49:45
Job time: 199 sec

Thu Aug 15 11:07:55 2002

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